



# Blast 2 Sequences results

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Structure



## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align

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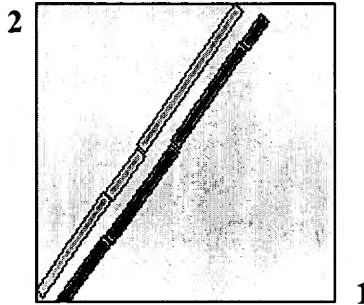
TECH CENTER 1600/2900

Sequence 1 lcl|seq\_1 Length 226 (1 .. 226)

Sequence 2 lcl|seq\_2 Length 160 (1 .. 160)

Seq No 3

HS FLI



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 73.6 bits (179), Expect = 4e-13

Identities = 48/155 (30%), Positives = 84/155 (53%), Gaps = 4/155 (2%)

Query: 21 LKNLKEINVGFNYLKSIPPELGDCENLERLDCSGNLELMELPFELSNLKQVTFVDISANK 80  
 L NL ++++ N L +P L +L RL+ S N ++ EL + V +++S N+  
 Sbjct: 1 LSNLADVLSNDLTRVPECLYTLPSLRRLNLSSN-QITELSLCIDQVHVETLNLSRNQ 59

Query: 81 FSSVPICVLRMSNLQWLDISSNNLT--DLPQDIDRLEELQSFLLYKNKLTYPYSMLNLK 138  
 +S+P + ++S L+ L ++SN L LP I +L L+ F+ N L +P S+  
 Sbjct: 60 LTSLPSAICKLSKLKKLYLNSNKLDGDFGSPGIGKLTNLEEFMAANNLELVPESLCRCP 119

Query: 139 KLTLVVSGDHLVELPTALCDSSTPLKFVSLMDNP 173  
 KL LV++ +HLV LP A+ T ++ + + +NP  
 Sbjct: 120 KLRKLVNLKNHLVTLPEAI-HFLTEIEVLDVREN 153

Score = 57.0 bits (136), Expect = 4e-08

Identities = 39/153 (25%), Positives = 83/153 (53%), Gaps = 3/153 (1%)

Query: 4 LDLPKNQISHLPAEIGCLKNLKEINVGFNYLKSIPPELGDCENLERLDCSGNLELMELPF 63  
 +DL N ++ +P + L +L+ LN+ N + + + ++E L+ S N +L LP  
 Sbjct: 7 VDLSCNDLTRVPECLYTLPSLRRLNLSSNQITELSLCIDQVHVETLNLSRN-QLTSLPS 65

Query: 64 ELSNLKQVTFVDISANK--FSSVPICVLRMSNLQWLDISSNNLTDLDPQDIDRLEELQSFL 121  
 + L ++ + +++NK F +P + +++NL+ ++NNL +P+ + R +L+ +  
 Sbjct: 66 AICKLSKLKKLYLNSNKLDGDFGSPGIGKLTNLEEFMAANNLELVPESLCRCPKLRKLV 125

Query: 122 LYKNKLTYPYSMLNLKKLTLVVSGDHLVELP 154

L KN L LP ++ L ++ +L V + + +P  
Sbjct: 126 LKNHNLVTLPEAIHFLTEIEVLVDVRENPNLVMP 158

CPU time: 0.08 user secs. 0.02 sys. secs 0.10 total secs.

Lambda	K	H
0.318	0.136	0.395

Gapped  
Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 547  
Number of Sequences: 0  
Number of extensions: 50  
Number of successful extensions: 15  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 6  
length of query: 160  
length of database: 324,428,749  
effective HSP length: 107  
effective length of query: 53  
effective length of database: 107,467,096  
effective search space: 5695756088  
effective search space used: 5695756088  
T: 9  
A: 40  
X1: 16 ( 7.3 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 41 (21.7 bits)  
S2: 64 (29.3 bits)